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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/367,052DATE: 01/05/2000
TIME: 13:10:51

Input Set: I367052.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: KISHIMOTO, Tadimitsu
2 NAGASAWA, Takashi
3 TACHIBANA, Kazunobu
4 IIZASA, Hisashi
5 YOSHIDA, Nobuaki
6 NAKAJIMA, Toshihiro
7 YOSHIE, Osamu
8 <120> TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
9 <130> FILE REFERENCE: 1422-386P
10 <140> CURRENT APPLICATION NUMBER: US/09/367,052
11 <141> CURRENT FILING DATE: 1999-08-06
12 <160> NUMBER OF SEQ ID NOS: 22
13 <170> SOFTWARE: PatentIn Ver. 2.0
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15 <211> LENGTH: 1877
16 <212> TYPE: DNA
17 <213> ORGANISM: Mus sp.
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23 tgaccctctg aggcgtttgg tgctccggta accaccacgg ctgtagagcg agtgttgcc 119
24 atg gaa ccg atc agt gtg agt ata tac act tct gat aac tac tct gaa 167
25 Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu
26 1 5 10 15
27 gaa gtg ggg tct gga gac tat gac tcc aac aag gaa ccc tgc ttc cgg 215
28 Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
29 20 25 30
30 gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc atc tac ttc 263
31 Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
32 35 40 45
33 atc atc ttc ttg act ggc ata gtc ggc aat gga ttg gtg atc ctg gtc 311
34 Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
35 50 55 60
36 atg ggt tac cag aag aag cta agg agc atg acg gac aag tac cgg ctg 359
37 Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
38 65 70 75 80
39 cac ctg tca gtg gct gac ctc ctc ttt gtc atc aca ctc ccc ttc tgg 407
40 His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
41 85 90 95
42 gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt aag 455
43 Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
44 100 105 110

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48      ctg gcc ttc atc agc ctg gac cgg tac ctc gcc att gtc cac gcc acc      551
49      Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
50              130                      135                      140
51      aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat gtg      599
52      Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
53      145                      150                      155                      160
54      ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc ttt      647
55      Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
56              165                      170                      175
57      gcc gac gtc agc cag ggg gac atc agt cag ggg gat gac agg tac atc      695
58      Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
59              180                      185                      190
60      tgt gac cgc ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc      743
61      Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
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63      cag cat ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc      791
64      Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
65              210                      215                      220
66      tgt tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag      839
67      Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
68      225                      230                      235                      240
69      aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc ttt      887
70      Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
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72      gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc atc      935
73      Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
74              260                      265                      270
75      ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg cac      983
76      Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
77              275                      280                      285
78      aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc ctg      1031
79      Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
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81      aac ccc atc ctc tat gcc ttc ctc ggg gcc aag ttc aaa agc tct gcc      1079
82      Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
83      305                      310                      315                      320
84      cag cat gca ctc aac tcc atg agc aga ggc tcc agc ctc aag atc ctt      1127
85      Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
86              325                      330                      335
87      tcc aaa gga aag cgg ggt gga cac tct tcc gtc tcc acg gag tca gaa      1175
88      Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
89              340                      345                      350
90      tcc tcc agt ttt cac tcc agc taacccttat gcaaagactt atataatata      1226
91      Ser Ser Ser Phe His Ser Ser
92              355
93      tatatatata tgataaagaa cttttttatg ttacacattt tccagatata agagactgac      1286
94      cagtcttgta cagttttttt ttttttttaa ttgactgttg ggagtttatg ttcctctagt      1346

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Input Set: I367052.RAW

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96      gcgtctaggc aggacctgtg gccaaagtct tagtagctgt ttatctgtgt gtaggactgt 1466
97      agaactgtag aggaagaaac tgaacattcc agaatgtgtg gtaaatgaa taaagctagc 1526
98      cgtgatcctc agctgttgct gcataatctc ttcattccga ggagcaccac acccccaccc 1586
99      ccacccccac cccattctta aattgttttg ttatgctgtg tgatggtttg tttggttttt 1646
100     ttttgttgtt gttgttgttt tttttttctg taaaagatgg cacttaaaac caaagcctga 1706
101     aatggtggta gaaatgctgg gggttttttt gttgtttgt tttttcagtt ttcaagagta 1766
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112           20             25             30
113     Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
114           35             40             45
115     Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
116           50             55             60
117     Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
118           65             70             75             80
119     His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
120           85             90             95
121     Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
122           100            105            110
123     Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
124           115            120            125
125     Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
126           130            135            140
127     Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
128           145            150            155            160
129     Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
130           165            170            175
131     Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
132           180            185            190
133     Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
134           195            200            205
135     Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
136           210            215            220
137     Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
138           225            230            235            240
139     Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
140           245            250            255
141     Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
142           260            265            270
143     Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
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147      Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
148          305                      310                      315                      320
149      Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
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165          1                      5                      10                      15
166      tgg gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt      96
167      Trp Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys
168          20                      25                      30
169      aag gct gtc cat atc atc tac act gtc aac ctc tac agc agc gtt ctc      144
170      Lys Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu
171          35                      40                      45
172      atc ctg gcc ttc atc agc ctg gac cgg tac ctc gcc att gtc cac gcc      192
173      Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala
174          50                      55                      60
175      acc aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat      240
176      Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr
177          65                      70                      75                      80
178      gtg ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc      288
179      Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile
180          85                      90                      95
181      ttt gcc gac gtc agc cag ggg gac atc agt cag ggg gat gac agg tac      336
182      Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr
183          100                      105                      110
184      atc tgt gac cgc ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa      384
185      Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln
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187      ttc cag cat ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc      432
188      Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu
189          130                      135                      140
190      tcc tgt tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac      480
191      Ser Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His
192          145                      150                      155                      160
193      cag aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc      528
194      Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe

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Input Set: I367052.RAW

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195          165          170          175
196      ttt gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc      576
197      Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe
198          180          185          190
199      atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg      624
200      Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val
201          195          200          205
202      cac aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc      672
203      His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys
204          210          215          220
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207      225          230
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216          20          25          30
217      Lys Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu
218          35          40          45
219      Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala
220          50          55          60
221      Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr
222          65          70          75          80
223      Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile
224          85          90          95
225      Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr
226          100          105          110
227      Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln
228          115          120          125
229      Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu
230          130          135          140
231      Ser Cys Tyr Cys Ile Ile Ser Lys Leu Ser His Ser Lys Gly His
232          145          150          155          160
233      Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
234          165          170          175
235      Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe
236          180          185          190
237      Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val
238          195          200          205
239      His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys
240          210          215          220
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242      225          230
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/367,052

DATE: 01/05/2000

TIME: 13:10:51

Input Set: I367052.RAW

Line ? Error/Warning

Original Text

467 W "N" or "Xaa" used: Feature required

ctsmgtttgk cmntnkcyga

483 W "N" or "Xaa" used: Feature required

tagaksanng grttsanrca rcagtg